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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: Thu Jun 07 17:57:20 EDT 2007

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Application No: 10728979

Version No: 1.0

Input Set:**Output Set:****Started:** 2007-06-07 09:28:31.766**Finished:** 2007-06-07 09:28:33.424**Elapsed:** 0 hr(s) 0 min(s) 1 sec(s) 658 ms**Total Warnings:** 38**Total Errors:** 0**No. of SeqIDs Defined:** 93**Actual SeqID Count:** 93

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W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
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W 213	Artificial or Unknown found in <213> in SEQ ID (9)
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W 213	Artificial or Unknown found in <213> in SEQ ID (17)
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W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
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Error Description

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<110> NEC CORPORATION
      MIYAKAWA, Tomoya
      NAKAZATO, Takeru
      ASOGAWA, Minoru

<120> Sequence Display Method and Homogeny Search Method

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<141> 2007-06-07

<150> JP 2002-358407
<151> 2002-12-10

<150> US 10/728,979
<151> 2003-12-08

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<170> PatentIn version 3.1

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<213> Artificial Sequence

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ggc ccg ccc tcc ccc gag gtc gga tcc cca ctg ctg tgt cgc cca gcc      96
Gly Pro Pro Ser Pro Glu Val Gly Ser Pro Leu Leu Cys Arg Pro Ala
          20          25          30

gca ggt ccg ttc ccg ggg agc cag acc tcg gac acc ttg cct gaa gtt      144
Ala Gly Pro Phe Pro Gly Ser Gln Thr Ser Asp Thr Leu Pro Glu Val
          35          40          45

tcg gcc ata cct atc tcc ctg gac ggg cta ctc ttc cct cgg ccc tgc      192
Ser Ala Ile Pro Ile Ser Leu Asp Gly Leu Leu Phe Pro Arg Pro Cys
          50          55          60

cag gga cag gac ccc tcc gac gaa aag acg cag gac cag cag tcg ctg      240
Gln Gly Gln Asp Pro Ser Asp Glu Lys Thr Gln Asp Gln Gln Ser Leu
65          70          75          80

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tcg gac gtg gag ggc gca tat tcc aga gct gaa gct aca agg ggt gct	288
Ser Asp Val Glu Gly Ala Tyr Ser Arg Ala Glu Ala Thr Arg Gly Ala	
85 90 95	
gga ggc agc agt tct agt ccc cca gaa aag gac agc gga ctg ctg gac	336
Gly Gly Ser Ser Ser Pro Pro Glu Lys Asp Ser Gly Leu Leu Asp	
100 105 110	
agt gtc ttg gac act ctg ttg gcg ccc tca ggt ccc ggg cag agc caa	384
Ser Val Leu Asp Thr Leu Leu Ala Pro Ser Gly Pro Gly Gln Ser Gln	
115 120 125	
ccc agc cct ccc gcc tgc gag gtc acc agc tct tgg tgc ctg ttt ggc	432
Pro Ser Pro Pro Ala Cys Glu Val Thr Ser Ser Trp Cys Leu Phe Gly	
130 135 140	
ccc gaa ctt ccc gaa gat cca ccg gct gcc ccc gcc acc cag cgg gtg	480
Pro Glu Leu Pro Glu Asp Pro Pro Ala Ala Pro Ala Thr Gln Arg Val	
145 150 155 160	
ttg tcc ccg ctc atg agc cgg tcc ggg tgc aag gtt gga gac agc tcc	528
Leu Ser Pro Leu Met Ser Arg Ser Gly Cys Lys Val Gly Asp Ser Ser	
165 170 175	
ggg acg gca gct gcc cat aaa gtg ctg ccc cgg ggc ctg tca cca gcc	576
Gly Thr Ala Ala Ala His Lys Val Leu Pro Arg Gly Leu Ser Pro Ala	
180 185 190	
cgg cag ctg ctg ctc ccg gcc tct gag agc cct cac tgg tcc ggg gcc	624
Arg Gln Leu Leu Leu Pro Ala Ser Glu Ser Pro His Trp Ser Gly Ala	
195 200 205	
cca gtg aag ccg tct ccg cag gcc gct gcg gtg gag gtt gag gag gag	672
Pro Val Lys Pro Ser Pro Gln Ala Ala Ala Val Glu Val Glu Glu Glu	
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gat agc tct gag tcc gag gag tct gcg ggt ccg ctt ctg aag ggc aaa	720
Asp Ser Ser Glu Ser Glu Glu Ser Ala Gly Pro Leu Leu Lys Gly Lys	
225 230 235 240	
cct cgg gct ctg ggt ggc gcg gcg gct gga gga gga gcc gcg gct tgt	768
Pro Arg Ala Leu Gly Gly Ala Ala Ala Gly Gly Gly Ala Ala Ala Cys	
245 250 255	
ccg ccg ggg gcg gca gca gga ggc gtc gcc ctg gtc ccc aag gaa gat	816
Pro Pro Gly Ala Ala Ala Gly Gly Val Ala Leu Val Pro Lys Glu Asp	
260 265 270	
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Ser Arg Phe Ser Ala Pro Arg Val Ala Leu Val Glu Gln Asp Ala Pro	
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Met Ala Pro Gly Arg Ser Pro Leu Ala Thr Thr Val Met Asp Phe Ile	
290 295 300	
cac gtg cct atc ctg cct ctc aat cac gcc tta ttg gca gcc cgc act	960

His Val Pro Ile Leu Pro Leu Asn His Ala Leu Leu Ala Ala Arg Thr	
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310	315
cgg cag ctg ctg gaa gac gaa agt tac gac ggc ggg gcc ggg gct gcc	1008
Arg Gln Leu Leu Glu Asp Glu Ser Tyr Asp Gly Gly Ala Gly Ala Ala	
325	330
335	
agc gcc ttt gcc ccg ccg cgg act tca ccc tgt gcc tcg tcc acc ccg	1056
Ser Ala Phe Ala Pro Pro Arg Thr Ser Pro Cys Ala Ser Ser Thr Pro	
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350	
gtc gct gta ggc gac ttc ccc gac tgc gcg tac ccg ccc gac gcc gag	1104
Val Ala Val Gly Asp Phe Pro Asp Cys Ala Tyr Pro Pro Asp Ala Glu	
355	360
365	
ccc aag gac gac gcg tac cct ctc tat agc gac ttc cag ccg ccc gct	1152
Pro Lys Asp Asp Ala Tyr Pro Leu Tyr Ser Asp Phe Gln Pro Pro Ala	
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cta aag ata aag gag gag gag gaa ggc gcg gag gcc tcc gcg cgc tcc	1200
Leu Lys Ile Lys Glu Glu Glu Glu Gly Ala Glu Ala Ser Ala Arg Ser	
385	390
395	400
ccg cgt tcc tac ctt gtg gcc ggt gcc aac ccc gca gcc ttc ccg gat	1248
Pro Arg Ser Tyr Leu Val Ala Gly Ala Asn Pro Ala Ala Phe Pro Asp	
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ttc ccg ttg ggg cca ccg ccc ccg ctg ccg ccg cga gcg acc cca tcc	1296
Phe Pro Leu Gly Pro Pro Pro Pro Leu Pro Pro Arg Ala Thr Pro Ser	
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430	
aga ccc ggg gaa gcg gcg gtg acg gcc gca ccc gcc agt gcc tca gtc	1344
Arg Pro Gly Glu Ala Ala Val Thr Ala Ala Pro Ala Ser Ala Ser Val	
435	440
445	
tcg tct gcg tcc tcc tcg ggg tcg acc ctg gag tgc atc ctg tac aaa	1392
Ser Ser Ala Ser Ser Ser Gly Ser Thr Leu Glu Cys Ile Leu Tyr Lys	
450	455
460	
gcg gag ggc gcg ccg ccc cag cag ggc ccg ttc gcg ccg ccg ccc tgc	1440
Ala Glu Gly Ala Pro Pro Gln Gln Gly Pro Phe Ala Pro Pro Pro Cys	
465	470
475	480
aag gcg ccg ggc gcg agc ggc tgc ctg ctc ccg cgg gac ggc ctg ccc	1488
Lys Ala Pro Gly Ala Ser Gly Cys Leu Leu Pro Arg Asp Gly Leu Pro	
485	490
495	
tcc acc tcc gcc tct gcc gcc gcc gcc ggg gcg gcc ccc gcg ctc tac	1536
Ser Thr Ser Ala Ser Ala Ala Ala Ala Gly Ala Ala Pro Ala Leu Tyr	
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515	520

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<212> PRT
<213> Artificial Sequence

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Ala Gly Pro Phe Pro Gly Ser Gln Thr Ser Asp Thr Leu Pro Glu Val
35 40 45

Ser Ala Ile Pro Ile Ser Leu Asp Gly Leu Leu Phe Pro Arg Pro Cys
50 55 60

Gln Gly Gln Asp Pro Ser Asp Glu Lys Thr Gln Asp Gln Gln Ser Leu
65 70 75 80

Ser Asp Val Glu Gly Ala Tyr Ser Arg Ala Glu Ala Thr Arg Gly Ala
85 90 95

Gly Gly Ser Ser Ser Ser Pro Pro Glu Lys Asp Ser Gly Leu Leu Asp
100 105 110

Ser Val Leu Asp Thr Leu Leu Ala Pro Ser Gly Pro Gly Gln Ser Gln
115 120 125

Pro Ser Pro Pro Ala Cys Glu Val Thr Ser Ser Trp Cys Leu Phe Gly
130 135 140

Pro Glu Leu Pro Glu Asp Pro Pro Ala Ala Pro Ala Thr Gln Arg Val
145 150 155 160

Leu Ser Pro Leu Met Ser Arg Ser Gly Cys Lys Val Gly Asp Ser Ser
165 170 175

Gly Thr Ala Ala Ala His Lys Val Leu Pro Arg Gly Leu Ser Pro Ala
180 185 190

Arg Gln Leu Leu Leu Pro Ala Ser Glu Ser Pro His Trp Ser Gly Ala
195 200 205

Pro Val Lys Pro Ser Pro Gln Ala Ala Ala Val Glu Val Glu Glu Glu
210 215 220

Asp Ser Ser Glu Ser Glu Glu Ser Ala Gly Pro Leu Leu Lys Gly Lys
225 230 235 240

Pro Arg Ala Leu Gly Gly Ala Ala Ala Gly Gly Gly Ala Ala Ala Cys
245 250 255

Pro Pro Gly Ala Ala Ala Gly Gly Val Ala Leu Val Pro Lys Glu Asp
260 265 270

Ser Arg Phe Ser Ala Pro Arg Val Ala Leu Val Glu Gln Asp Ala Pro
275 280 285

Met Ala Pro Gly Arg Ser Pro Leu Ala Thr Thr Val Met Asp Phe Ile
290 295 300

His Val Pro Ile Leu Pro Leu Asn His Ala Leu Leu Ala Ala Arg Thr
305 310 315 320

Arg Gln Leu Leu Glu Asp Glu Ser Tyr Asp Gly Gly Ala Gly Ala Ala
325 330 335

Ser Ala Phe Ala Pro Pro Arg Thr Ser Pro Cys Ala Ser Ser Thr Pro
340 345 350

Val Ala Val Gly Asp Phe Pro Asp Cys Ala Tyr Pro Pro Asp Ala Glu
355 360 365

Pro Lys Asp Asp Ala Tyr Pro Leu Tyr Ser Asp Phe Gln Pro Pro Ala
370 375 380

Leu Lys Ile Lys Glu Glu Glu Glu Gly Ala Glu Ala Ser Ala Arg Ser
385 390 395 400

Pro Arg Ser Tyr Leu Val Ala Gly Ala Asn Pro Ala Ala Phe Pro Asp
405 410 415

Phe Pro Leu Gly Pro Pro Pro Pro Leu Pro Pro Arg Ala Thr Pro Ser

420

425

430

Arg Pro Gly Glu Ala Ala Val Thr Ala Ala Pro Ala Ser Ala Ser Val
 435 440 445

Ser Ser Ala Ser Ser Ser Gly Ser Thr Leu Glu Cys Ile Leu Tyr Lys
 450 455 460

Ala Glu Gly Ala Pro Pro Gln Gln Gly Pro Phe Ala Pro Pro Pro Cys
 465 470 475 480

Lys Ala Pro Gly Ala Ser Gly Cys Leu Leu Pro Arg Asp Gly Leu Pro
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<213> Artificial Sequence

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<211> 60

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<210> 6

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<210> 7

<211> 60

<212> DNA

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